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#8

## SEQUENCE LISTING

<110> Anderson, Marilyn, A., Lay, Fung T., Heath, Robyn, L.

<120> Plant-derived molecules and genetic sequences encoding same and uses therefor

<130> 18-01

<140> USSN 10/072,809

<141> 2002-02-08

<150> USSN 60/267,271

<151> 2001-02-08

<160> 61

<170> PatentIn version 3.0

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<223> Description of Artificial Sequence: Primer

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 Arg Glu Cys Lys Thr Glu Ser Asn Thr Phe Pro Gly Ile Cys Ile Thr  
 1 5 10 15  
  
 aaa cca cca tgc aga aaa gct tgt atc agt gag aaa ttt act gat ggt 96  
 Lys Pro Pro Cys Arg Lys Ala Cys Ile Ser Glu Lys Phe Thr Asp Gly  
 20 25 30  
  
 cat tgt agc aaa atc ctc aga agg tgc cta tgt act aag cca tgt 141  
 His Cys Ser Lys Ile Leu Arg Arg Cys Leu Cys Thr Lys Pro Cys  
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 ctc ttt gtt gcc tat gag gtg caa gct 75  
 Leu Phe Val Ala Tyr Glu Val Gln Ala  
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 gaa gca aaa act ttg gct gca gct ttg ctt gaa gaa gag ata atg gat 96  
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1 5 10 15

ctc ttt gtt gcc tat gag gtg caa gct aga gaa tgc aaa aca gaa agc 96  
Leu Phe Val Ala Tyr Glu Val Gln Ala Arg Glu Cys Lys Thr Glu Ser  
20 25 30

aac aca ttt cct gga ata tgc att acc aaa cca cca tgc aga aaa gct 144  
Asn Thr Phe Pro Gly Ile Cys Ile Thr Lys Pro Pro Cys Arg Lys Ala  
35 40 45

tgt atc agt gag aaa ttt act gat ggt cat tgt agc aaa atc ctc aga 192  
Cys Ile Ser Glu Lys Phe Thr Asp Gly His Cys Ser Lys Ile Leu Arg  
50 55 60

agg tgc cta tgt act aag cca tgt 216  
Arg Cys Leu Cys Thr Lys Pro Cys  
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1 5 10 15

aaa cca cca tgc aga aaa gct tgt atc agt gag aaa ttt act gat ggt 96  
Lys Pro Pro Cys Arg Lys Ala Cys Ile Ser Glu Lys Phe Thr Asp Gly  
20 25 30

cat tgt agc aaa atc ctc aga agg tgc cta tgt act aag cca tgt gtg 144  
His Cys Ser Lys Ile Leu Arg Arg Cys Leu Cys Thr Lys Pro Cys Val  
35 40 45

ttt gat gag aag atg act aaa aca gga gct gaa att ttg gct gag gaa 192  
Phe Asp Glu Lys Met Thr Lys Thr Gly Ala Glu Ile Leu Ala Glu Glu  
50 55 60

gca aaa act ttg gct gca gct ttg ctt gaa gaa gag ata atg gat aac 240  
Ala Lys Thr Leu Ala Ala Leu Leu Glu Glu Glu Ile Met Asp Asn  
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Lys Pro Pro Cys Arg Lys Ala Cys Ile Ser Glu Lys Phe Thr Asp Gly  
20 25 30

His Cys Ser Lys Ile Leu Arg Arg Cys Leu Cys Thr Lys Pro Cys Val  
35 40 45

Phe Asp Glu Lys Met Thr Lys Thr Gly Ala Glu Ile Leu Ala Glu Glu  
 50 55 60

Ala Lys Thr Leu Ala Ala Ala Leu Leu Glu Glu Glu Ile Met Asp Asn  
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 1 5 10 15

ctc ttt gtt gcc tat gag gtg caa gct aga gaa tgc aaa aca gaa agc 96  
 Leu Phe Val Ala Tyr Glu Val Gln Ala Arg Glu Cys Lys Thr Glu Ser  
 20 25 30

aac aca ttt cct gga ata tgc att acc aaa cca cca tgc aga aaa gct 144  
 Asn Thr Phe Pro Gly Ile Cys Ile Thr Lys Pro Pro Cys Arg Lys Ala  
 35 40 45

tgt atc agt gag aaa ttt act gat ggt cat tgt agc aaa atc ctc aga 192  
 Cys Ile Ser Glu Lys Phe Thr Asp Gly His Cys Ser Lys Ile Leu Arg  
 50 55 60

agg tgc cta tgt act aag cca tgt gtg ttt gat gag aag atg act aaa 240  
 Arg Cys Leu Cys Thr Lys Pro Cys Val Phe Asp Glu Lys Met Thr Lys  
 65 70 75 80

aca gga gct gaa att ttg gct gag gaa gca aaa act ttg gct gca gct 288  
 Thr Gly Ala Glu Ile Leu Ala Glu Glu Ala Lys Thr Leu Ala Ala Ala  
 85 90 95

ttg ctt gaa gaa gag ata atg gat aac taa ttagagatta gaagaaatta 338  
 Leu Leu Glu Glu Glu Ile Met Asp Asn  
 100 105

aggatgcagt atcacacata ataaagtttc tacctttctt aaaagtgtag ctaatgttgt 398

gttttaattg gcttttagta gccttttatt acacttttaa taagtgtggc acttcaatcc 458

tttgtgcaat cttgcactaa gtttatttgt gtacttttaa tgaaaatgac cttctatggt 518

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Asn Thr Phe Pro Gly Ile Cys Ile Thr Lys Pro Pro Cys Arg Lys Ala  
35 40 45  
Cys Ile Ser Glu Lys Phe Thr Asp Gly His Cys Ser Lys Ile Leu Arg  
50 55 60  
Arg Cys Leu Cys Thr Lys Pro Cys Val Phe Asp Glu Lys Met Thr Lys  
65 70 75 80  
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taagtgtggc acttcaatcc tttgtgcaat cttgcactaa gtttatttgt gtacttttaa 180  
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Asn Thr Phe Pro Gly Ile Cys Ile Thr Lys Pro Pro Cys Arg Lys Ala  
35 40 45  
Cys Ile Ser Glu Lys Phe Thr Asp Gly His Cys Ser Lys Leu Leu Arg  
50 55 60  
Arg Cys Leu Cys Thr Lys Pro Cys Val Phe Asp Glu Lys Met Ile Lys  
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Thr Gly Ala Glu Thr Leu Val Glu Glu Ala Lys Thr Leu Ala Ala Ala  
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Leu Leu Glu Glu Glu Ile Met Asp Asn  
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Leu Phe Val Thr Tyr Glu Val Glu Ala Gln Gln Ile Cys Lys Ala Pro  
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Ser Gln Thr Phe Pro Gly Leu Cys Phe Met Asp Ser Ser Cys Arg Lys  
35 40 45

Tyr Cys Ile Lys Glu Lys Phe Thr Gly Gly His Cys Ser Lys Leu Gln  
50 55 60

Arg Lys Cys Leu Cys Thr Lys Pro Cys Val Phe Asp Lys Ile Ser Ser  
65 70 75 80

Glu Val Lys Ala Thr Leu Gly Glu Glu Ala Lys Thr Leu Ser Glu Val  
85 90 95

Val Leu Glu Glu Glu Ile Met Met Glu  
100 105

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<211> 78  
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Leu Val Thr Ala Thr Glu Met Gly Pro Met Thr Ile Ala Glu Ala Arg  
20 25 30

Thr Cys Glu Ser Gln Ser His Arg Phe Lys Gly Pro Cys Ser Arg Asp  
35 40 45

Ser Asn Cys Ala Thr Val Cys Leu Thr Glu Gly Phe Ser Gly Gly Arg  
50 55 60

Cys Pro Trp Ile Pro Pro Arg Cys Phe Cys Thr Ser Pro Cys  
65 70 75

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<211> 78  
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<400> 23  
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Leu Phe Leu Ser Thr Glu Met Gly Pro Met Thr Ser Ala Glu Ala Arg  
20 25 30  
Thr Cys Glu Ser Gln Ser His Arg Phe His Gly Thr Cys Val Arg Glu  
35 40 45  
Ser Asn Cys Ala Ser Val Cys Gln Thr Glu Gly Phe Ile Gly Gly Asn  
50 55 60  
Cys Arg Ala Phe Arg Arg Arg Cys Phe Cys Thr Arg Asn Cys  
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Ile Phe Val Ala Thr Gly Met Gly Pro Val Thr Val Glu Ala Arg Thr  
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Cys Glu Ser Gln Ser His Arg Phe Lys Gly Thr Cys Val Ser Ala Ser  
35 40 45  
Asn Cys Ala Asn Val Cys His Asn Glu Gly Phe Val Gly Gly Asn Cys  
50 55 60  
Arg Gly Phe Arg Arg Arg Cys Phe Cys Thr Arg His Cys  
65 70 75

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Lys Pro Pro Cys Arg Lys Ala Cys Ile Ser Glu Lys Phe Thr Asp Gly  
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His Cys Ser Lys Leu Leu Arg Arg Cys Leu Cys Thr Lys Pro Cys  
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 Asp Ser Ser Cys Arg Lys Tyr Cys Ile Lys Glu Lys Phe Thr Gly Gly  
 20 25 30  
 His Cys Ser Lys Leu Gln Arg Lys Cys Leu Cys Thr Lys Pro Cys  
 35 40 45

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<400> 27  
 Arg His Cys Glu Ser Leu Ser His Arg Phe Lys Gly Pro Cys Thr Arg  
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 Asp Ser Asn Cys Ala Ser Val Cys Glu Thr Glu Arg Phe Ser Gly Gly  
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 Asn Cys His Gly Phe Arg Arg Arg Cys Phe Cys Thr Lys Pro Cys  
 35 40 45

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 Asp His Asn Cys Ala Leu Val Cys Arg Asn Glu Gly Phe Ser Gly Gly  
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 Arg Cys Lys Gly Phe Arg Arg Arg Cys Phe Cys Thr Arg Ile Cys  
 35 40 45

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35 40 45

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His Gly Ser Cys Asn Tyr Val Phe Pro Ala His Lys Cys Ile Cys Tyr  
35 40 45  
Phe Pro Cys  
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<210> 33  
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<400> 33  
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His Gly Ser Cys Asn Tyr Val Phe Pro Ala His Lys Cys Ile Cys Tyr  
 35 40 45

Phe Pro Cys  
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His Gly Ser Cys Asn Tyr Val Phe Pro Ala His Lys Cys Ile Cys Tyr  
 35 40 45

Phe Pro Cys  
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His Gly Ser Cys Asn Tyr Val Phe Pro Ala His Lys Cys Ile Cys Tyr  
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Phe Pro Cys  
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Arg His Gly Ser Cys Asn Ile Pro Phe Pro Ser Asn Lys Cys Ile Cys  
 35 40 45

Tyr Phe Pro Cys  
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Asn Cys Asp Gly Pro Phe Arg Arg Cys Lys Cys Ile Arg Gln Cys  
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Asp Lys Asn Cys Ala Gln Val Cys Leu Gln Glu Gly Trp Gly Gly Gly  
20 25 30

Asn Cys Asp Gly Pro Phe Arg Arg Cys Lys Cys Ile Arg Gln Cys  
35 40 45

<210> 39  
<211> 47  
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<400> 39  
Lys Thr Cys Glu Asn Leu Val Asp Thr Tyr Arg Gly Pro Cys Phe Thr  
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20 25 30

Gly Arg Cys Arg Asp Asp Val Arg Cys Trp Cys Thr Arg Asn Cys  
35 40 45

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<211> 48  
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Asn Cys Asp Gly Val Met Arg Gln Cys Lys Cys Ile Arg Gln Cys Trp  
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Asn Cys Asp Gly Val Ile Arg Gln Cys Lys Cys Ile Arg Gln Cys Trp  
35 40 45

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Thr Gly His Cys  
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<211> 47  
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Asp Arg Leu Cys Ser Asn Glu Cys Val Lys Glu Glu Gly Gly Trp Thr  
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35 40 45

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<211> 45  
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Cys Arg Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys  
 35 40 45

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Thr Ala His Cys Asp Lys Gln Cys Gln Asp Trp Glu Lys Ala Ser His  
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Gly Ala Cys His Lys Arg Glu Asn His Trp Lys Cys Phe Cys Tyr Phe  
 35 40 45

Asn Cys  
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<210> 46  
 <211> 51  
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<400> 46  
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Ser Ser Lys Cys Ser Gln Gln Cys Lys Asp Arg Glu His Phe Ala Tyr  
 20 25 30

Gly Gly Ala Cys His Tyr Gln Phe Pro Ser Val Lys Cys Phe Cys Lys  
 35 40 45

Arg Gln Cys  
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 <211> 50  
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<400> 47  
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 1 5 10 15

Thr Gly His Cys Asp Asn Gln Cys Lys Ser Trp Glu Gly Ala Ala His  
 20 25 30

Gly Ala Cys His Val Arg Asn Gly Lys His Met Cys Phe Cys Tyr Phe  
 35 40 45



Asn Cys  
50

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Gly Thr Cys His Asp Trp Lys Cys Phe Cys Thr Gln Asn Cys  
35 40 45

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Thr Gly His Cys Asp Thr Gln Cys Arg Asn Trp Glu Ser Ala Lys His  
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Gly Ala Cys His Lys Arg Gly Asn Trp Lys Cys Phe Cys Tyr Phe Asn  
35 40 45

Cys

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20 25 30

Lys Glu Lys Phe Thr Asp Gly His Cys Ser Lys Ile Leu Arg Arg Cys  
35 40 45

Leu Cys Thr Lys Pro Cys Thr Gly Ala Glu Thr Leu Ala Glu Glu Ala  
50 55 60

Thr Thr Leu Ala Ala Ala Leu Leu Glu Glu Glu Ile Met Asp Asn  
65 70 75

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 35 40 45  
 Cys Ile Lys Glu Lys Phe Thr Asp Gly His Cys Ser Lys Ile Leu Arg  
 50 55 60  
 Arg Cys Leu Cys Thr Lys Pro Cys Val Phe Asp Glu Lys Met Ile Lys  
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 Leu Leu Glu Glu Glu Ile Met Asp Asn  
 100 105

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 35 40 45  
 Ala Cys Leu Ser Glu Lys Phe Thr Asp Gly Lys Cys Ser Lys Ile Leu  
 50 55 60  
 Arg Arg Cys Ile Cys Tyr Lys Pro Cys Val Phe Asp Gly Lys Met Ile  
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48

ccg cgt tca gaa gaa aag aag aat gat cgg ata tgc acc aac tgt tgc Pro Arg Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys 20 25 30	96
gca ggc acg aag ggt tgt aag tac ttc agt gat gat gga act ttt gtt Ala Gly Thr Lys Lys Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val 35 40 45	144
tgt gaa gga gag tct gat cct aga aat cca aag gct tgt acc tta aac Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Ala Cys Thr Leu Asn 50 55 60	192
tgt gat cca aga att gcc tat gga gtt tgc cgg cgt tca gaa gaa aag Cys Asp Pro Arg Ile Ala Tyr Gly Val Cys Pro Arg Ser Glu Glu Lys 65 70 75 80	240
aag aat gat cgg ata tgc acc aac tgt tgc gca ggc acg aag ggt tgt Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Thr Lys Gly Cys 85 90 95	288
aag tac ttc agt gat gat gga act ttt gtt tgt gaa gga gag tct gat Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val Cys Glu Gly Glu Ser Asp 100 105 110	336
cct aga aat cca aag gct tgt cct cgg aat tgc gat cca aga att gcc Pro Arg Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp Pro Arg Ile Ala 115 120 125	384
tat ggg att tgc cca ctt gca gaa gaa aag aag aat gat cgg ata tgc Tyr Gly Ile Cys Pro Leu Ala Glu Glu Lys Lys Asn Asp Arg Ile Cys 130 135 140	432
acc aac tgt tgc gca ggc aaa aag ggt tgt aag tac ttt agt gat gat Thr Asn Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp 145 150 155 160	480
gga act ttt gtt tgt gaa gga gag tct gat cct aaa aat cca aag gcc Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Lys Asn Pro Lys Ala 165 170 175	528
tgt cct cgg aat tgt gat gga aga att gcc tat ggg att tgc cca ctt Cys Pro Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu 180 185 190	576
tca gaa gaa aag aag aat gat cgg ata tgc acc aac tgc tgc gca ggc Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly 195 200 205	624
aaa aag ggt tgt aag tac ttt agt gat gat gga act ttt gtt tgt gaa Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val Cys Glu 210 215 220	672
gga gag tct gat cct aaa aat cca aag gct tgt cct cgg aat tgt gat Gly Glu Ser Asp Pro Lys Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp 225 230 235 240	720

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Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn	
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gat cgg ata tgc aca aac tgt tgc gca ggc aaa aag ggc tgt aag tac	816
Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr	
260 265 270	
ttt agt gat gat gga act ttt gtt tgt gaa gga gag tct gat cct aga	864
Phe Ser Asp Asp Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Arg	
275 280 285	
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Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly	
290 295 300	
att tgc cca ctt tca gaa gaa aag aag aat gat cgg ata tgc acc aat	960
Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn	
305 310 315 320	
tgt tgc gca ggc aag aag ggc tgt aag tac ttt agt gat gat gga act	1008
Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr	
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ttt att tgt gaa gga gaa tct gaa tat gcc agc aaa gtg gat gaa tat	1056
Phe Ile Cys Glu Gly Glu Ser Glu Tyr Ala Ser Lys Val Asp Glu Tyr	
340 345 350	
gtt ggt gaa gtg gag aat gat ctc cag aag tct aag gtt gct gtt tcc	1104
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35 40 45	
Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Ala Cys Thr Leu Asn	
50 55 60	
Cys Asp Pro Arg Ile Ala Tyr Gly Val Cys Pro Arg Ser Glu Glu Lys	
65 70 75 80	

Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Thr Lys Gly Cys  
85 90 95

Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val Cys Glu Gly Glu Ser Asp  
100 105 110

Pro Arg Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp Pro Arg Ile Ala  
115 120 125

Tyr Gly Ile Cys Pro Leu Ala Glu Glu Lys Lys Asn Asp Arg Ile Cys  
130 135 140

Thr Asn Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp  
145 150 155 160

Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Lys Asn Pro Lys Ala  
165 170 175

Cys Pro Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu  
180 185 190

Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly  
195 200 205

Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val Cys Glu  
210 215 220

Gly Glu Ser Asp Pro Lys Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp  
225 230 235 240

Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn  
245 250 255

Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr  
260 265 270

Phe Ser Asp Asp Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Arg  
275 280 285

Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly  
290 295 300

Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn  
 305 310 315 320

Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr  
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Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Glu Xaa Phe Xaa Xaa Gly
          20          25          30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Thr Xaa Xaa Cys
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa
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